

Estimation of genomic breeding values for traits with high and low heritability in Brown Swiss bulls



M. Kramer¹, F. Biscarini¹, B. Bapst², C. Stricker³, H. Simianer¹

¹ Department of Animal Sciences, Animal Breeding and Genetics Group,
Georg-August-University Göttingen, Germany

² QUALITAS AG, Zug, Switzerland

³ agn Genetics GmbH, Davos, Switzerland



Outline



- Introduction, aim of the study
- Material and methods
 - Data, Filtering, imputing
 - Different G matrices
- Results
 - logL with different G matrices
 - Accuracy of gEBVs with different G matrices
- Conclusions

Introduction



- GBLUP is a common approach for estimation of genomic breeding values (gEBVs)
 - Regression on SNP effects
 - Use of genomic relationship matrix (G matrix)

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 - Regression on SNP effects
 - Use of genomic relationship matrix (G matrix)
- Several methods are well known in animal breeding for setting up G matrices from SNP data
 - Hayes and Goddard (2008)
 - Van Raden (2008)

Aim of the Study



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 - ⇒ Comparison of G matrix by Astle and Balding (2009) to widely used algorithms
 - logL as a measurement of how well the model fits the data
 - Accuracy of gEBVs from different G matrices compared by cross validation

Material



- 1,138 Brown Swiss bulls
- 54,001 SNP genotypes (Illumina 54k SNP Chip)
- Conventional EBVs (April 2010):
 - Milk yield (MY)
 - Somatic cell score (SCS)
 - Non-return rate (NRR)
 - Interval from calving to first insemination (CFI)

Filtering and imputation



- Elimination of SNP markers:
 - Unknown position
 - Callrate $< 95\%$
 - MAF $< 5\%$
- ⇒ 34,474 SNP used for analysis
- Imputing with BEAGLE 3.2
(Browning and Browning, 2009)

Statistical model



- GBLUP in ASReml:

$$\mathbf{y} = \mathbf{1}\boldsymbol{\mu} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

\mathbf{y} vector of EBVs

$$\mathbf{u} \sim N(\mathbf{0}, \mathbf{G}\sigma_u^2)$$

$$\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}\sigma_e^2)$$

Cross validation



- 5 fold cross validation with 10 replicates
- Random distribution of animals to validation and calibration set
 - All accuracies are means of 50 replicates
- Calculation of accuracy (Legarra et al. 2008):

$$r(g, \hat{g}) = \frac{r(y, \hat{g})}{\sqrt{h^2}}$$

Different G matrices



- **Hayes and Goddard (2008):**

$$\bar{S}_{xy} = \frac{S_{xy} - \min}{1 - \min}$$

- Where S_{xy} is the average **similarity index** (Eding and Meuwissen, 2001) over all loci

$$S_{xy,l} = \frac{I_{11} + I_{12} + I_{21} + I_{22}}{4}$$

Different G matrices



- **Van Raden (2008):**

$$\mathbf{G}_{\text{VR}} = \frac{\mathbf{ZZ}'}{2 \sum p_l (1 - p_l)}$$

- **Astle and Balding (2009):**

$$\mathbf{G}_{\text{AB}} = \frac{1}{L} \sum \frac{(\mathbf{z}_{.,l})(\mathbf{z}_{.,l})'}{4 p_l (1 - p_l)}$$

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relationship

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kinship

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Average over **all** loci

Each locus **individually**

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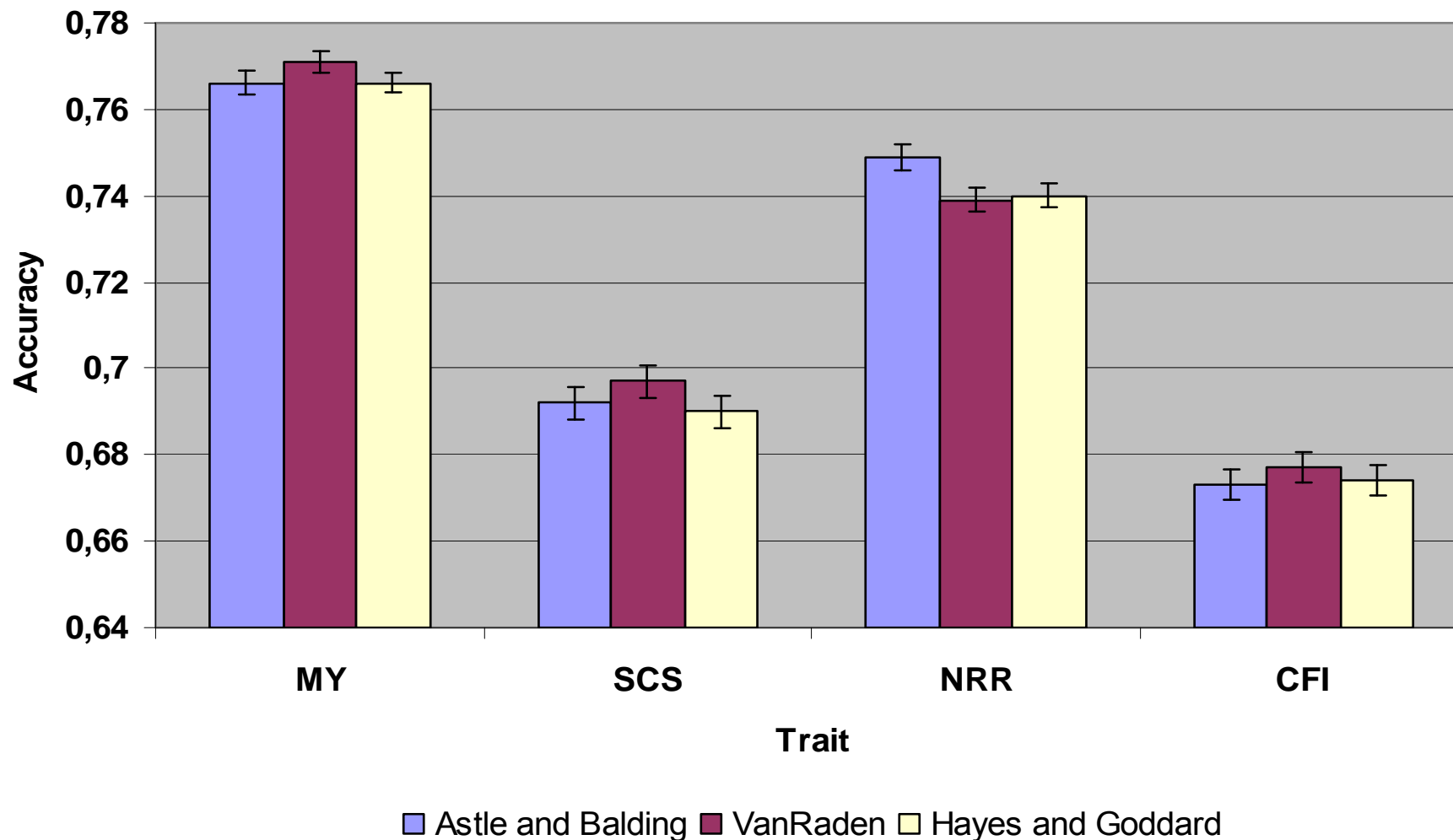
Results -logL of the model



G matrix	logL MY	logL SCS	logL NRR	logL CFI
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Astle & Balding	-7218.55	-2917.51	-2706.86	-3050.14
VanRaden	-7227.55	-2921.61	-2710.88	-3052.30
Hayes & Goddard	-7227.92	-2921.61	-2709.76	-3052.30

Results -accuracy of gEBVs



Conclusion



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Conclusion



- G matrix by Astle and Balding can be used to estimate gEBVs.
- G matrix by Astle and Balding delivers higher logL than G matrix by VanRaden or G Matrix by Hayes and Goddard
 - Fitting of the model with G matrix by Astle and Balding is the best
- **Accuracies of gEBVs are equivalent with all three G matrices**

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Thanks for Your attention!



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